Figure 1.

1 acquire data

2 process signal

3 separate colors

4 remove primers

5 track sizes

6 extract profiles

Figure 2.

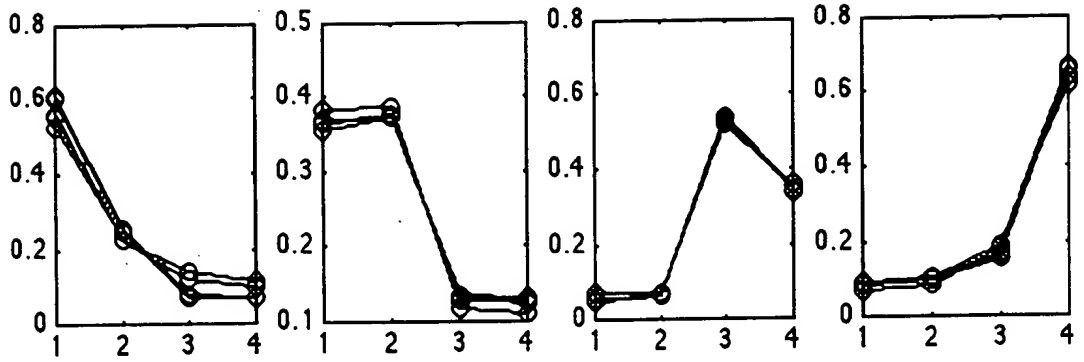
0.8
0.6
0.4
0.2
0
1 2 3 4
0.5
0.4
0.3
0.2
0.1
1 2 3 4
0.8
0.6
0.4
0.2
0
1 2 3 4
0.8
0.6
0.4
0.2
0
1 2 3 4

Figure 3.

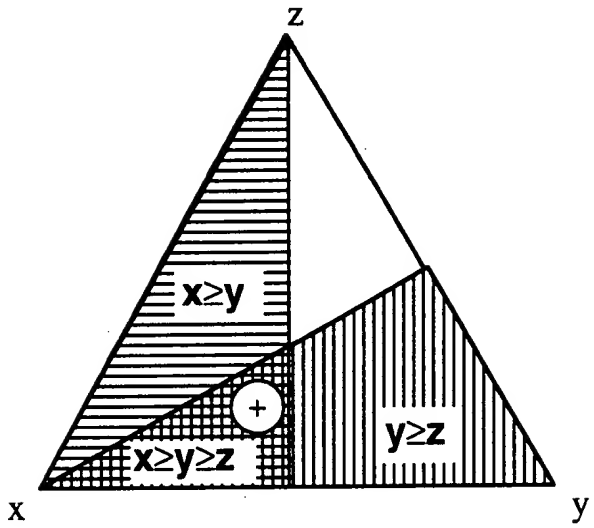

Figure 4.

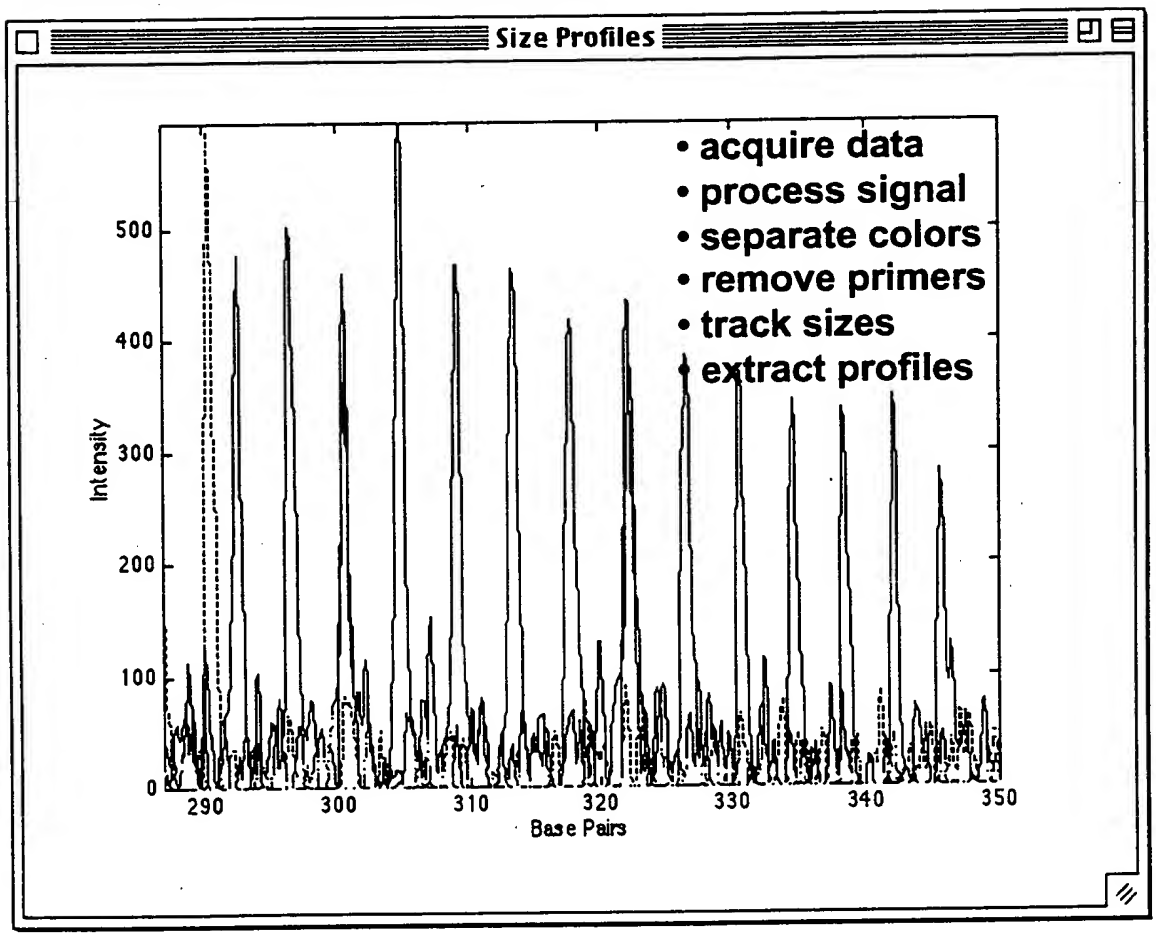
Size Profiles
• acquire data
• process signal
• separate colors
• remove primers
• track sizes
• extract profiles
Intensity
0
100
200
300
400
500
290
300
310
320
330
340
350
Base Pairs

Figure 5.

7 derive allelic ladder

8 transform coordinates

9 quantitate trace

10 analyze data

Figure 6.

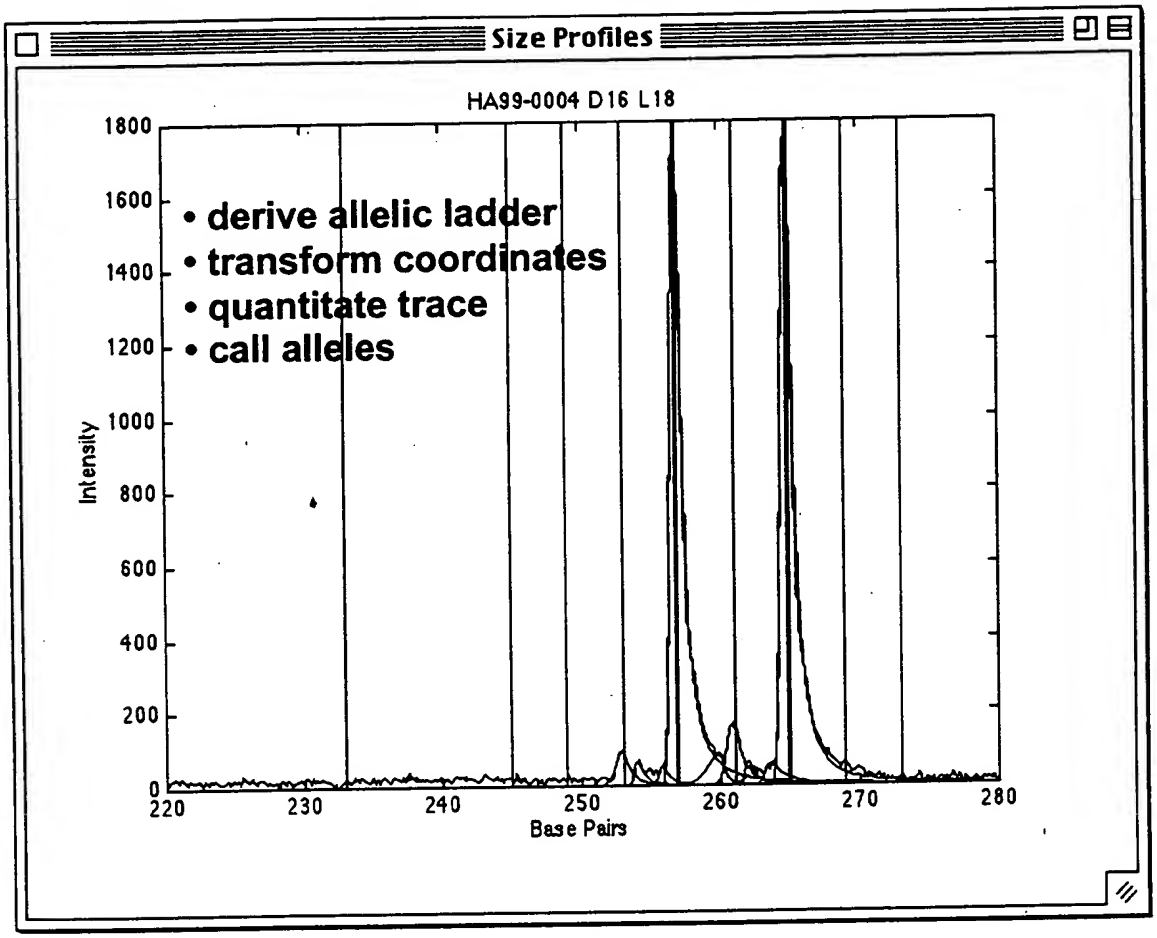
Size Profiles
HA99-0004 D16 L18
• derive allelic ladder
• transform coordinates
• quantitate trace
• call alleles
Intensity
1800
1600
1400
1200
1000
800
600
400
200
0
220
230
240
250
260
270
280
Base Pairs

Figure 7.

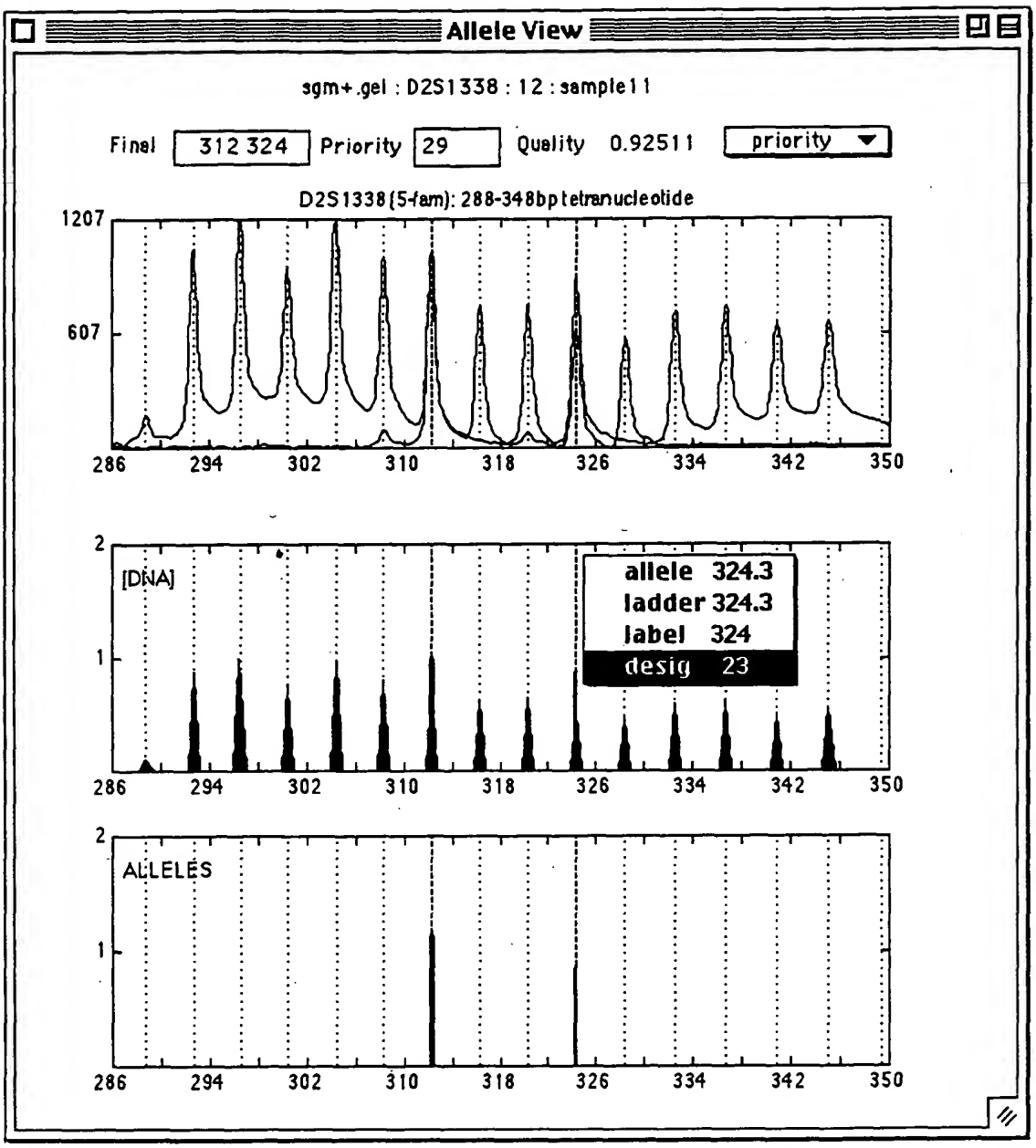
Allele View
sgm+.gel : D2S1338 : 12 : sample11
Final 312 324
Priority 29
Quality 0.92511
priority
D2S1338(5-fam): 288-348bp tetranucleotide
1207
607
286 294 302 310 318 326 334 342 350
[DNA]
allele 324.3
ladder 324.3
label 324
desig 23
ALLELES

Figure 8.

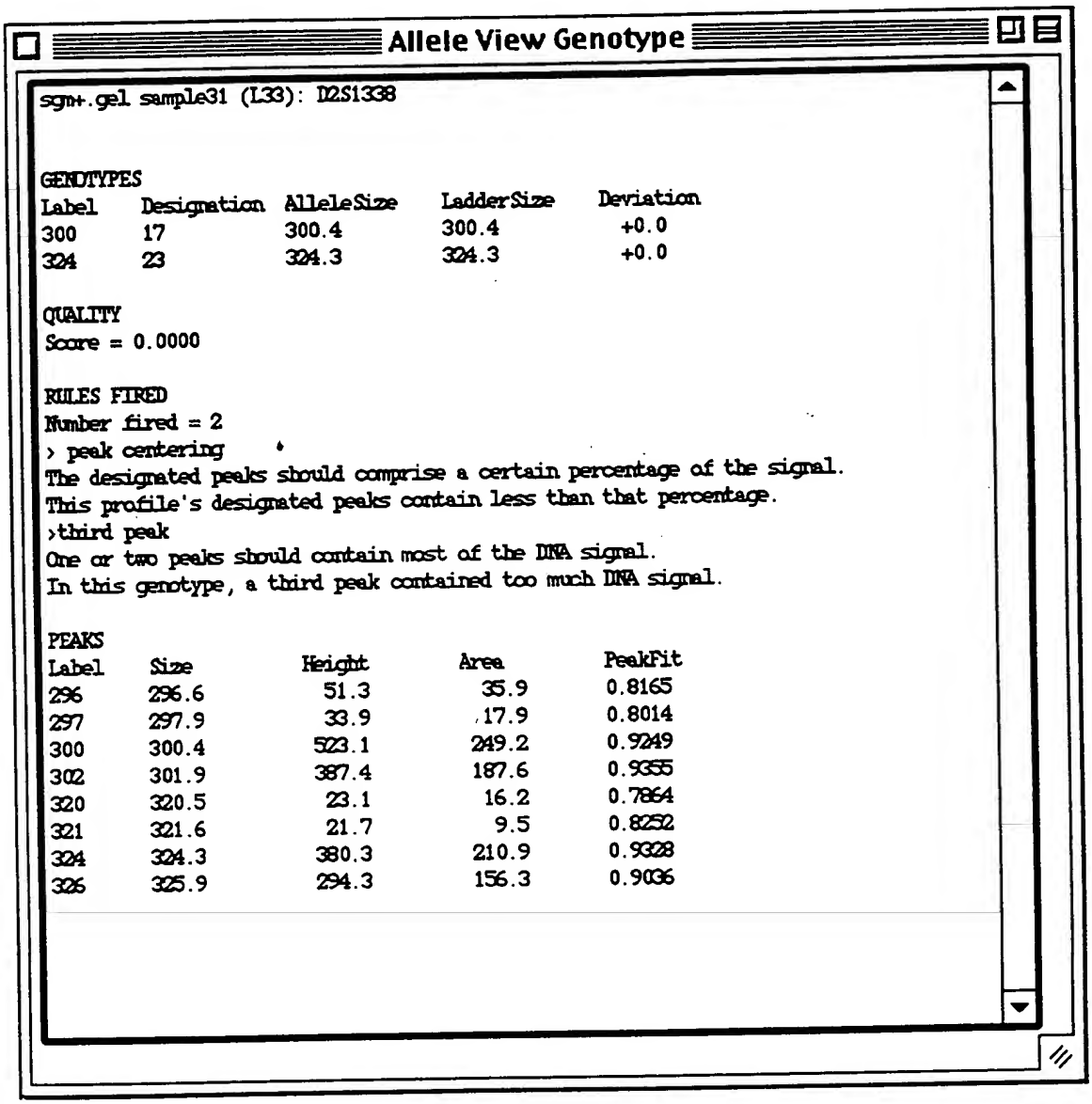
Allele View Genotype
sgm+.gel sample31 (L33): D2S1338
GENOTYPES
Label Designation AlleleSize LadderSize Deviation
300 17 300.4 300.4 +0.0
324 23 324.3 324.3 +0.0
QUALITY
Score = 0.0000
RULES FIRED
Number fired = 2
› peak centering
The designated peaks should comprise a certain percentage of the signal.
This profile's designated peaks contain less than that percentage.
›third peak
One or two peaks should contain most of the DNA signal.
In this genotype, a third peak contained too much DNA signal.
PEAKS
Label Size Height Area PeakFit
296 296.6 51.3 35.9 0.8165
297 297.9 33.9 17.9 0.8014
300 300.4 523.1 249.2 0.9249
302 301.9 387.4 187.6 0.9355
320 320.5 23.1 16.2 0.7864
321 321.6 21.7 9.5 0.8252
324 324.3 380.3 210.9 0.9328
326 325.9 294.3 156.3 0.9036

Figure 9.

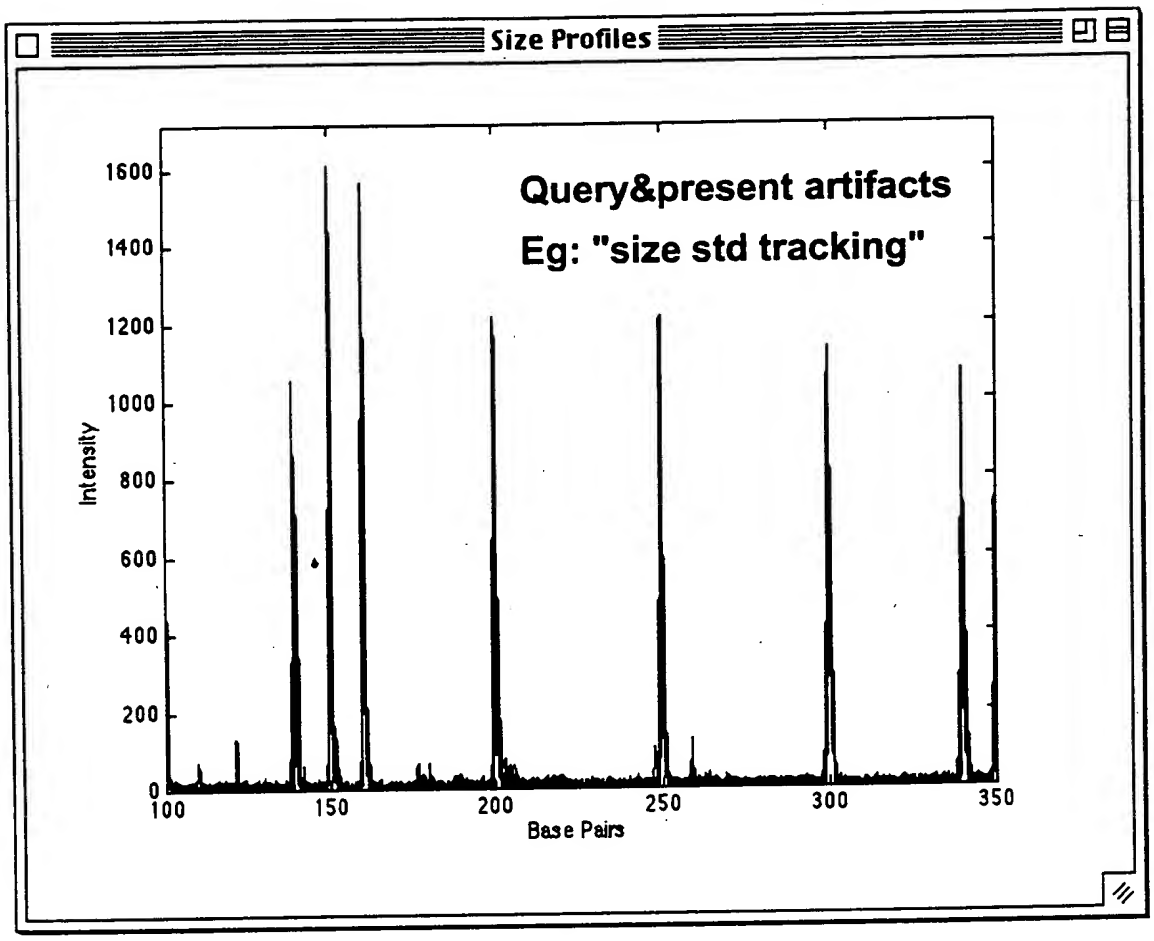
Size Profiles
Query&present artifacts
Eg: "size std tracking"
Intensity
1600
1400
1200
1000
800
600
400
200
0
100
150
200
250
300
350
Base Pairs

Figure 10.

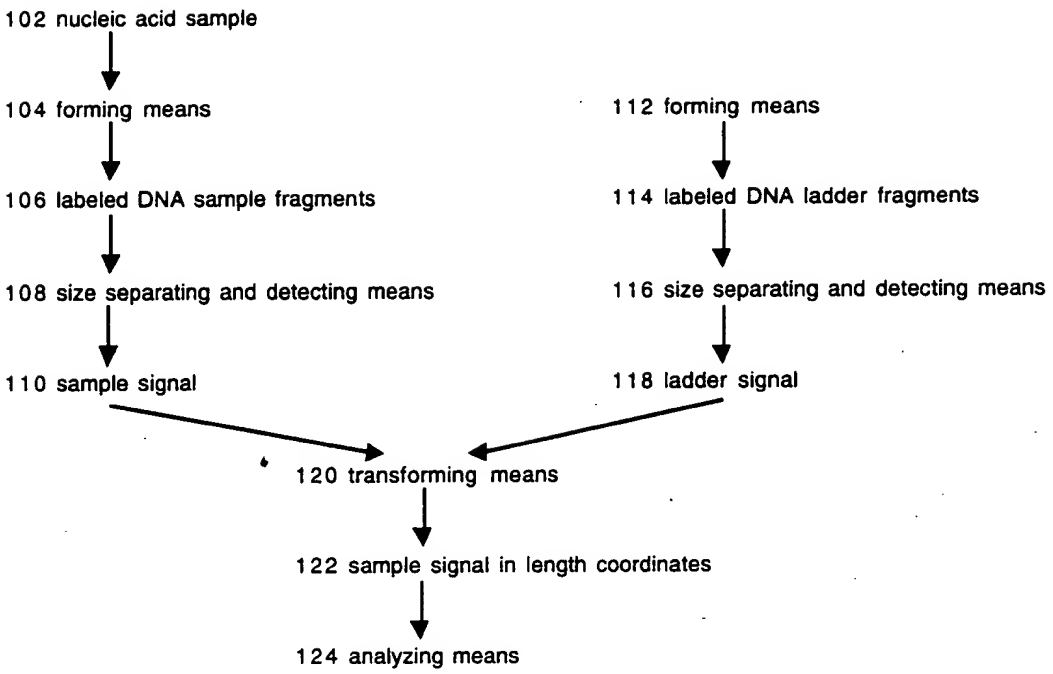
102 nucleic acid sample
104 forming means
106 labeled DNA sample fragments
108 size separating and detecting means
110 sample signal
112 forming means
114 labeled DNA ladder fragments
116 size separating and detecting means
118 ladder signal
120 transforming means
122 sample signal in length coordinates
124 analyzing means

Figure 11.

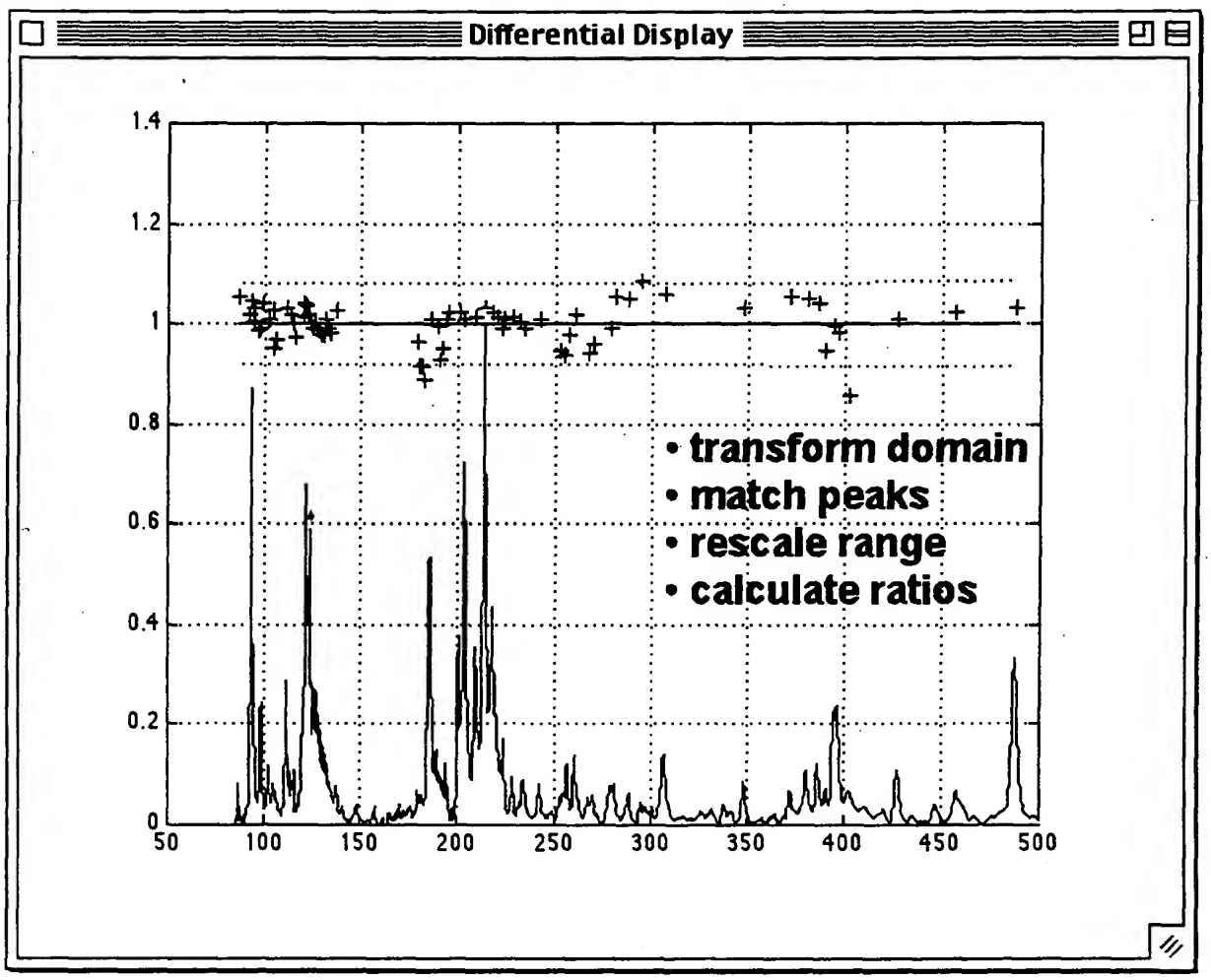
Differential Display
1.4
1.2
1
0.8
0.6
0.4
0.2
0
50
100
150
200
250
300
350
400
450
500
• transform domain
• match peaks
• rescale range
• calculate ratios

Figure 12

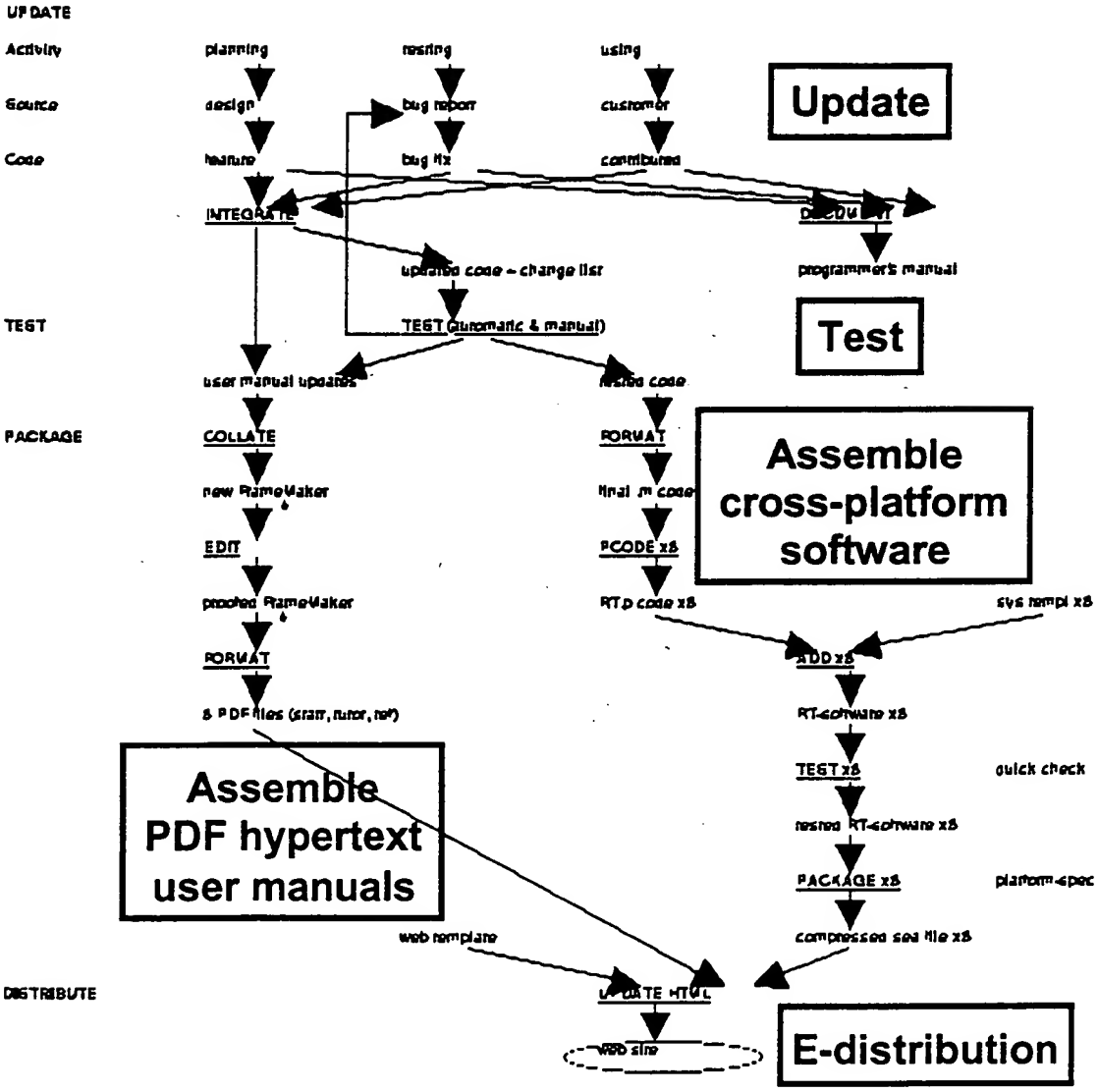
UPDATE
Activity
planning
testing
using
Source
design
bug report
customer
Code
feature
bug fix
commitment
Update
INTEGRATE
DOCUMENT
updated code + change list
programmer's manual
TEST
TEST (automatic & manual)
Test
user manual updates
tested code
PACKAGE
COLLATE
FORMAT
Assemble cross-platform software
new FrameMaker
final .m code
EDIT
PCODE x8
proofed FrameMaker
RTp code x8
sys rempi x8
FORMAT
ADD x8
8 PDF files (gram, tutor, ref)
RT-software x8
Assemble PDF hypertext user manuals
TEST x8
quick check
tested RT-software x8
PACKAGE x8
platform-spec
web template
compressed sea file x8
DISTRIBUTE
UPDATE HTML
web site
E-distribution

Figure 13

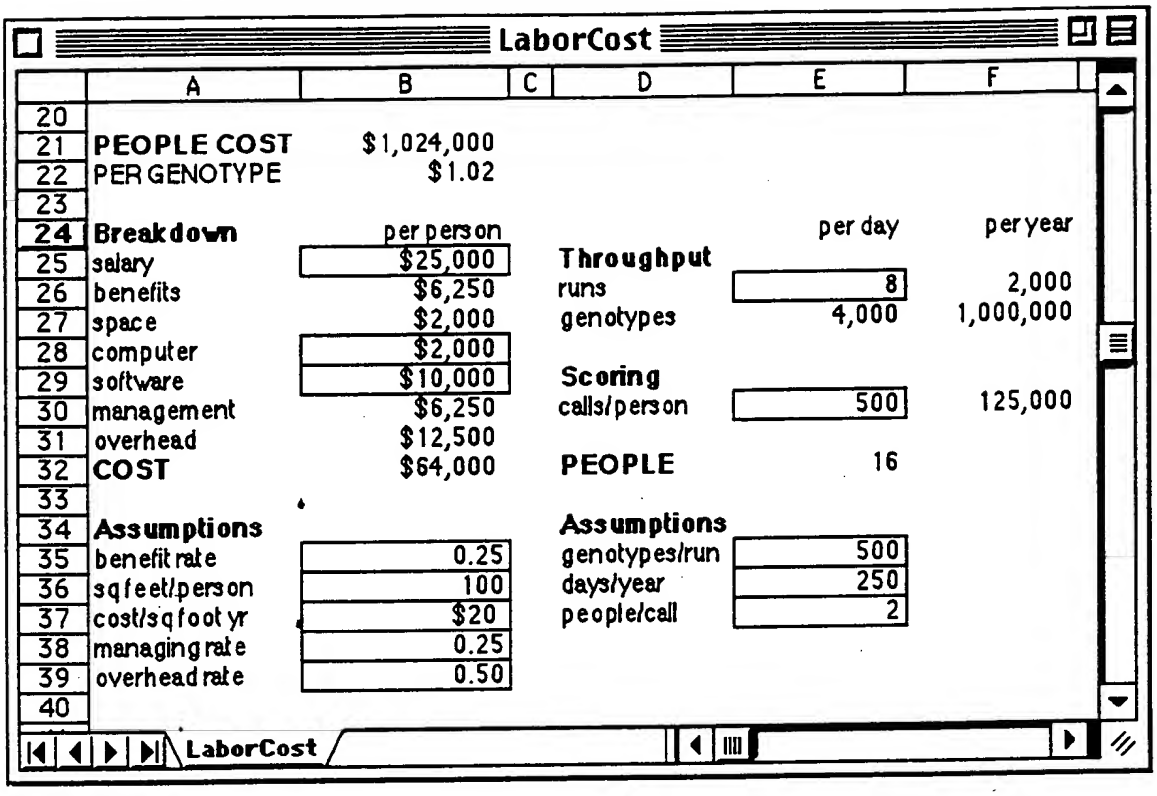
LaborCost
A
B
C
D
E
F
20
21 PEOPLE COST $1,024,000
22 PER GENOTYPE $1.02
23
24 Breakdown per person
25 salary $25,000
26 benefits $6,250
27 space $2,000
28 computer $2,000
29 software $10,000
30 management $6,250
31 overhead $12,500
32 COST $64,000
33
34 Assumptions
35 benefit rate 0.25
36 sq feet/person 100
37 cost/sq foot yr $20
38 managing rate 0.25
39 overhead rate 0.50
40
per day
per year
Throughput
runs 8 2,000
genotypes 4,000 1,000,000
Scoring
calls/person 500 125,000
PEOPLE 16
Assumptions
genotypes/run 500
days/year 250
people/call 2
LaborCost

Figure 14.